

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANTS: Clinton, Gail M., Doherty, Joni Kristin, and Adelman, John P.

(ii) TITLE OF INVENTION: HER-2 BINDING ANTAGONISTS

(iii) NUMBER OF SEQUENCES: 10

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: DAVIS WRIGHT TREMAINE

(B) STREET: 1501 Fourth Avenue, 2600 Century Square

(C) CITY: Seattle

(D) STATE: Washington

(E) COUNTRY: U.S.A.

(F) ZIP: 98101

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk

(B) COMPUTER: PC compatible

(C) OPERATING SYSTEM: Windows95

(D) SOFTWARE: Word

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: to be assigned

(B) FILING DATE: February 16, 2000

(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Oster, Jeffrey B.

(B) REGISTRATION NUMBER: 32,585

(C) REFERENCE/DOCKET NUMBER: 49321-1

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 206 628 7711

(B) TELEFAX: 206 628 7699

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 79

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: HER-2 ECD antagonist

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

00505079-031500

Gly	Xaa	His	Ser	Xaa	Xaa	Pro	Arg	Pro	Ala	Ala	Val	Pro	Val	Pro	Xaa
				5					10					15	
Arg	Xaa	Gln	Pro	Xaa	Pro	Ala	His	Pro	Val	Leu	Ser	Phe	Leu	Arg	Pro
			20					25					30		
Ser	Trp	Asp	Xaa	Val	Ser	Ala	Phe	Tyr	Ser	Leu	Pro	Leu	Ala	Pro	Leu
		35					40					45			
Ser	Pro	Thr	Ser	Val	Xaa	Ile	Ser	Pro	Val	Ser	Val	Gly	Arg	Gly	Xaa
	50					55					60				
Asp	Pro	Asp	Ala	His	Val	Ala	Val	Xaa	Leu	Ser	Arg	Tyr	Glu	Gly	
65					70					75					

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 419

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: polypeptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met	Glu	Leu	Ala	Ala	Leu	Cys	Arg	Trp	Gly	Leu	Leu	Leu	Ala	Leu	Leu
				5					10					15	
Pro	Pro	Gly	Ala	Ala	Ser	Thr	Gln	Val	Cys	Thr	Gly	Thr	Asp	Cys	Lys
				20					25					30	
Leu	Arg	Leu	Pro	Ala	Ser	Pro	Glu	Thr	His	Leu	Asp	Met	Leu	Arg	His
			35					40					45		
Leu	Tyr	Gln	Gly	Cys	Gln	Val	Val	Gln	Gly	Asn	Leu	Glu	Leu	Thr	Tyr
	50						55					60			
Leu	Pro	Thr	Asn	Ala	Ser	Leu	Ser	Phe	Leu	Gln	Asp	Ile	Gln	Glu	Val
	65					70					75				
Gln	Gly	Tyr	Val	Leu	Cys	Ala	His	Asn	Gln	Val	Arg	Gln	Val	Pro	Leu
80					85					90				95	
Gln	Arg	Leu	Arg	Ile	Val	Arg	Gly	Thr	Gln	Leu	Phe	Glu	Asp	Asn	Tyr
				100					105					110	
Ala	Leu	Ala	Val	Leu	Asp	Asn	Gly	Asp	Pro	Leu	Agn	Agn	Thr	Thr	Pro
			115					120					125		
Val	Thr	Gly	Ala	Ser	Pro	Gly	Gly	Leu	Arg	Glu	Leu	Gln	Leu	Arg	Ser
		130					135						140		
Leu	Thr	Glu	Cys	Leu	Lys	Gly	Gly	Val	Leu	Ile	Gln	Arg	Asn	Pro	Gln
	145					150					155				
Leu	Cys	Tyr	Gln	Asp	Thr	Ile	Leu	Trp	Lys	Asp	Ile	Phe	His	Lys	Asn
160					165					170				175	
Asn	Gln	Leu	Ala	Leu	Thr	Leu	Ile	Asp	Thr	Asn	Arg	Ser	Arg	Ala	Cys
				180						185				190	
His	Pro	Cys	Ser	Pro	Cys	Cys	Lys	Gly	Ser	Arg	Cys	Trp	Gly	Glu	Ser

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			195					200					205				
Ser	Glu	Asp	Cys	Gln	Ser	Leu	Thr	Arg	Thr	Val	Cys	Ala	Gly	Gly	Cys		
		210						215					220				
Ala	Arg	Cys	Lys	Gly	Pro	Leu	Pro	Thr	Asp	Cys	Cys	His	Glu	Gln	Cys		
		225						230					235				
Ala	Ala	Gly	Cys	Thr	Gly	Pro	Lys	His	Ser	Asp	Cys	Leu	Ala	Cys	Leu		
		240						245					250				255
His	Phe	Asn	His	Ser	Gly	Ile	Cys	Glu	Leu	His	Cys	Pro	Ala	Leu	Val		
				260						265					270		
Thr	Tyr	Asn	Thr	Asp	Thr	Phe	Glu	Ser	Cys	Pro	Asn	Pro	Glu	Gly	Arg		
				275					280						285		
Tyr	Thr	Phe	Gly	Ala	Ser	Cys	Val	Thr	Ala	Cys	Pro	Tyr	Asn	Lys	Leu		
		290						295					300				
Ser	Thr	Asp	Val	Gly	Ser	Cys	Thr	Leu	Val	Cys	Pro	Leu	His	Asn	Gln		
		305						310					315				
Glu	Val	Thr	Ala	Glu	Asp	Gly	Thr	Gln	Arg	Cys	Glu	Lys	Cys	Ser	Lys		
		320						325					330				335
Pro	Cys	Ala	Arg	Val	Gly	Xaa	His	Ser	Xaa	Xaa	Pro	Arg	Pro	Ala	Ala		
				340						345					350		
Val	Pro	Val	Pro	Xaa	Arg	Xaa	Gln	Pro	Xaa	Pro	Ala	His	Pro	Val	Leu		
			355					360					365				
Ser	Phe	Leu	Arg	Pro	Ser	Trp	Asp	Xaa	Val	Ser	Ala	Phe	Tyr	Ser	Leu		
		370						375					380				
Pro	Leu	Ala	Pro	Leu	Asp	Pro	Thr	Ser	Val	Xaa	Ile	Ser	Pro	Val	Ser		
		385						390					395				
Val	Gly	Arg	Gly	Xaa	Asp	Pro	Asp	Ala	His	Val	Ala	Val	Xaa	Leu	Ser		
		400					405				410				415		
Arg	Tyr	Glu	Gly														

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 19
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: oligonucleotide
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

TGAGCACCAT GGAGCTGGC 19

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 22
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single

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- (D) TOPOLOGY: unknown  
(ii) MOLECULE TYPE: oligonucleotide  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

TCCGGCAGAA ATGCCAGGCT CC 22

- (2) INFORMATION FOR SEQ ID NO:5:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 22  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: unknown  
(ii) MOLECULE TYPE: oligonucleotide  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

AACACAGCGG TGTGAGAAGT GC 22

- (2) INFORMATION FOR SEQ ID NO:6:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 21  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: unknown  
(ii) MOLECULE TYPE: oligonucleotide  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

ATACCGGGAC AGGTCAACAG C 21

- (2) INFORMATION FOR SEQ ID NO:7:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 20  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: unknown  
(ii) MOLECULE TYPE: oligonucleotide  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

TCTGGGTACC CACTCACTGC 20

- (2) INFORMATION FOR SEQ ID NO:8:  
(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 22  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: unknown  
(ii) MOLECULE TYPE: oligonucleotide

005720-02090500

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

TTCACACTGG CACGTCCAGA CC 22

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GCACGGATCC ATAGCAGACT GAGGAGG 27

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 240 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

GGT	WCC	CAC	TCA	CYG	CYC	CCG	AGG	COA	GCT	GCA	GTT	CCT	GTC	CCT	45
Gly	Xaa	His	Ser	Xaa	Xaa	Pro	Arg	Pro	Ala	Ala	Val	Pro	Val	Pro	
				5					10					15	
CWG	CGC	ATR	CAG	CCT	GNC	CCA	GCC	CAC	CCT	GTC	CTA	TCC	TTC	CTC	90
Xaa	Arg	Xaa	Gln	Pro	Xaa	Pro	Ala	His	Pro	Val	Leu	Ser	Phe	Leu	
				20					25					30	
AGA	CCC	TCT	TGG	GAC	MTA	GTC	TCT	GCC	TTC	TAC	TCT	CTA	CCC	CTG	135
Arg	Pro	Ser	Trp	Asp	Xaa	Val	Ser	Ala	Phe	Tyr	Ser	Leu	Pro	Leu	
				35					40					45	
GCC	CCC	CTC	AGC	CCT	ACA	AGT	GTC	CST	ATA	TCC	CCT	GTC	AGT	GTG	180
Ala	Pro	Leu	Ser	Pro	Thr	Ser	Val	Xaa	Ile	Ser	Pro	Val	Ser	Val	
				50					55					60	
GGG	AGG	GGC	CYG	GAC	CCT	GAT	GCT	CAT	GTG	GCT	GTT	SAC	CTG	TCC	225
Gly	Arg	Gly	Xaa	Asp	Pro	Asp	Ala	His	Val	Ala	Val	Xaa	Leu	Ser	
				65					70					75	
CGG	TAT	GAA	GGC	TGA											240
Arg	Tyr	Glu	Gly												

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